0570
1023

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RAW SEQUENCE LISTING DATE: 10/24/2001
PATENT APPLICATION: US/09/724,685 TIME: 12:35:47

Input Set : A:\-85-6-1.app
Output Set: N:\CRF3\10242001\I724685.raw

SEQUENCE LISTING

ENTERED

(1) GENERAL INFORMATION:

(i) APPLICANT: Reed, Steven G.
Skeiky, Yasir
Dillon, Davin C.
Campos-Neto, Antonio

(ii) TITLE OF INVENTION: Compounds and Methods for
Immunotherapy and Diagnosis of Tuberculosis

(iii) NUMBER OF SEQUENCES: 155

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Townsend and Townsend and Crew LLP
(B) STREET: Two Embarcadero Center, Eighth Floor
(C) CITY: San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94111-3834

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
C--> **(A) APPLICATION NUMBER: US/09/724,685**
C--> **(B) FILING DATE: 28-Nov-2000**
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/523,436
(B) FILING DATE: 01-SEP-1995
(A) APPLICATION NUMBER: US 08/533,634
(B) FILING DATE: 22-SEP-1995
(A) APPLICATION NUMBER: US 08/620,874
(B) FILING DATE: 22-MAR-1996
(A) APPLICATION NUMBER: US 08/659,683
(B) FILING DATE: 05-JUN-1996
(A) APPLICATION NUMBER: US 08/680,574
(B) FILING DATE: 12-JUL-1996
(A) APPLICATION NUMBER: WO PCT/US96/14674
(B) FILING DATE: 30-AUG-1996
(A) APPLICATION NUMBER: US 08/730,511
(B) FILING DATE: 11-OCT-1996
(A) APPLICATION NUMBER: US 08/818,112
(B) FILING DATE: 13-MAR-1997

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Bastian, Kevin L.
(B) REGISTRATION NUMBER: 34,774
(C) REFERENCE/DOCKET NUMBER: 014058-008561US

(ix) TELECOMMUNICATION INFORMATION:

RAW SEQUENCE LISTING DATE: 10/24/2001
PATENT APPLICATION: US/09/724,685 TIME: 12:35:47

Input Set : A:\-85-6-1.app
Output Set: N:\CRF3\10242001\I724685.raw

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73          (A) TELEPHONE: (415) 576-0200
74          (B) TELEFAX: (415) 576-0300
77 (2) INFORMATION FOR SEQ ID NO: 1:
79      (i) SEQUENCE CHARACTERISTICS:
80          (A) LENGTH: 766 base pairs
81          (B) TYPE: nucleic acid
82          (C) STRANDEDNESS: single
83          (D) TOPOLOGY: linear
85     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
87 CGAGGCACCG GTAGTTTGAA CCAAACGCAC AATCGACGGG CAAACGAACG GAAGAACACA      60
89 ACCATGAAGA TGGTGAAATC GATCGCCGCA GGTCTGACCG CCGCGGCTGC AATCGGCGCC     120
91 GCTGCGGCCG GTGTGACTTC GATCATGGCT GGCGGCCCGG TCGTATACCA GATGCAGCCG     180
93 GTCGTCTTCG GCGCGCCACT GCCGTTGGAC CCGGCATCCG CCCCTGACGT CCCGACCGCC     240
95 GCCCAGTTGA CCAGCCTGCT CAACAGCCTC GCCGATCCCA ACGTGTCGTT TGCGAACAAG     300
97 GGCAGTCTGG TCGAGGGCGG CATCGGGGGC ACCGAGGCGC GCATCGCCGA CCACAAGCTG     360
99 AAGAAGGCCG CCGAGCACGG GGATCTGCCG CTGTCGTTCA GCGTGACGAA CATCCAGCCG     420
101 GCGGCCGCCG GTTCGGCCAC CGCCGACGTT TCCGTCTCGG GTCCGAAGCT CTCGTCGCCG     480
103 GTCACGCAGA ACGTCACGTT CGTGAATCAA GGCGGCTGGA TGCTGTCACG CGCATCGGCG     540
105 ATGGAGTTGC TGCAGGCCGC AGGGNAACTG ATTGGCGGGC CGGNTTCAGC CCGCTGTTCA     600
107 GCTACGCCGC CCGCCTGGTG ACGCGTCCAT GTCGAACACT CGCGCGTGTA GCACGGTGCG     660
109 GTNTGCGCAG GGNCGCACGC ACCGCCCGGT GCAAGCCGTC CTCGAGATAG GTGGTGNCTC     720
111 GNCACCAGNG ANCACCCCCN NNTCGNCNNT TCTCGNTGNT GNATGA                   766
114 (2) INFORMATION FOR SEQ ID NO: 2:
116      (i) SEQUENCE CHARACTERISTICS:
117          (A) LENGTH: 752 base pairs
118          (B) TYPE: nucleic acid
119          (C) STRANDEDNESS: single
120          (D) TOPOLOGY: linear
122     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
124 ATGCATCACC ATCACCATCA CGATGAAGTC ACGGTAGAGA CGACCTCCGT CTTCCGCGCA      60
126 GACTTCCTCA GCGAGCTGGA CGCTCCTGCG CAAGCGGGTA CGGAGAGCGC GGTCTCCGGG     120
128 GTGGAAGGGC TCCCGCCGGG CTCGGCGTTG CTGGTAGTCA AACGAGGCCC CAACGCCGGG     180
130 TCCCGGTTCC TACTCGACCA AGCCATCACG TCGGCTGGTC GGCATCCCGA CAGCGACATA     240
132 TTTCTCGACG ACGTGACCGT GAGCCGTCGC CATGCTGAAT TCCGGTTGGA AAACAACGAA     300
134 TTCAATGTCG TCGATGTCGG GAGTCTCAAC GGCACCTACG TCAACCGCGA GCCCGTGGAT     360
136 TCGGCGGTGC TGGCGAACGG CGACGAGGTC CAGATCGGCA AGCTCCGGTT GGTGTTCTTG     420
138 ACCGGACCCA AGCAAGGCGA GGATGACGGG AGTACCGGGG GCCCGTGAGC GCACCCGATA     480
140 GCCCCGCGCT GGCCGGGATG TCGATCGGGG CGGTCCTCCG ACCTGCTACG ACCGGATTTT     540
142 CCCTGATGTC CACCATCTCC AAGATTCGAT TCTTGGGAGG CTTGAGGGTC NGGGTGACCC     600
144 CCCCGCGGGC CTCATTCNGG GGTNTCGGCN GGTTTCACCC CNTACCNACT GCCNCCCGGN     660
146 TTGCNAATTC NTTCTTCNCT GCCCNNAAAG GGACCNTTAN CTTGCCGCTN GAAANGGTNA     720
148 TCCNGGGCCC NTCCTNGAAN CCCCNTCCCC CT                                   752
151 (2) INFORMATION FOR SEQ ID NO: 3:
153      (i) SEQUENCE CHARACTERISTICS:
154          (A) LENGTH: 813 base pairs
155          (B) TYPE: nucleic acid
156          (C) STRANDEDNESS: single
157          (D) TOPOLOGY: linear
159     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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Input Set : A:\-85-6-1.app
Output Set: N:\CRF3\10242001\I724685.raw

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161 CATATGCATC ACCATCACCA TCACACTTCT AACCGCCCAG CGCGTCGGGG GCGTCGAGCA      60
163 CCACGCGACA CCGGGCCCGA TCGATCTGCT AGCTTGAGTC TGGTCAGGCA TCGTCGTCAG     120
165 CAGCGCGATG CCCTATGTTT GTCGTCGACT CAGATATCGC GGCAATCCAA TCTCCCGCCT     180
167 GCGGCCGGCG GTGCTGCAAA CTACTCCCGG AGGAATTTCG ACGTGCGCAT CAAGATCTTC     240
169 ATGCTGGTCA CGGCTGTCGT TTTGCTCTGT TGTTCGGGTG TGGCCACGGC CGCGCCCAAG     300
171 ACCTACTGCG AGGAGTTGAA AGGCACCGAT ACCGGCCAGG CGTGCCAGAT TCAAATGTCC     360
173 GACCCGGCCT ACAACATCAA CATCAGCCTG CCCAGTTACT ACCCCGACCA GAAGTCGCTG     420
175 GAAAATTACA TCGCCCAGAC GCGCGACAAG TTCCTCAGCG CGGCCACATC GTCCACTCCA     480
177 CGCGAAGCCC CCTACGAATT GAATATCACC TCGGCCACAT ACCAGTCCGC GATACCGCCG     540
179 CGTGGTACGC AGGCCGTGGT GCTCAMGGTC TACCACAACG CCGGCGGCAC GCACCCAACG     600
181 ACCACGTACA AGGCCTTCGA TTGGGACCAG GCCTATCGCA AGCCAATCAC CTATGACACG     660
183 CTGTGGCAGG CTGACACCGA TCCGCTGCCA GTCGTCTTCC CCATTGTTGC AAGGTGAACT     720
185 GAGCAACGCA GACCGGGACA ACWGGTATCG ATAGCCGCCN AATGCCGGCT TGGAACCCNG     780
187 TGAAATTATC ACAACTTCGC AGTCACNAAA NAA                                  813
190 (2) INFORMATION FOR SEQ ID NO: 4:
192      (i) SEQUENCE CHARACTERISTICS:
193           (A) LENGTH: 447 base pairs
194           (B) TYPE: nucleic acid
195           (C) STRANDEDNESS: single
196           (D) TOPOLOGY: linear
198     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
200 CGGTATGAAC ACGGCCGCGT CCGATAACTT CCAGCTGTCC CAGGGTGGGC AGGGATTCGC      60
202 CATTCCGATC GGGCAGGCGA TGGCGATCGC GGGCCAGATC CGATCGGGTG GGGGGTCACC     120
204 CACCGTTCAT ATCGGGCCTA CCGCCTTCCT CGGCTTGGGT GTTGTCGACA ACAACGGCAA     180
206 CGGCGCACGA GTCCAACGCG TGGTCGGGAG CGCTCCGGCG GCAAGTCTCG GCATCTCCAC     240
208 CGGCGACGTG ATCACCGCGG TCGACGGCGC TCCGATCAAC TCGGCCACCG CGATGGCGGA     300
210 CGCGCTTAAC GGGCATCATC CCGGTGACGT CATCTCGGTG AACTGGCAAA CCAAGTCGGG     360
212 CGGCACGCGT ACAGGGAACG TGACATTGGC CGAGGGACCC CCGGCCTGAT TTCGTCGYGG     420
214 ATACCACCCG CCGGCCGGCC AATTGGA                                         447
217 (2) INFORMATION FOR SEQ ID NO: 5:
219      (i) SEQUENCE CHARACTERISTICS:
220           (A) LENGTH: 604 base pairs
221           (B) TYPE: nucleic acid
222           (C) STRANDEDNESS: single
223           (D) TOPOLOGY: linear
225     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
227 GTCCCACTGC GGTCGCCGAG TATGTCGCCC AGCAAATGTC TGGCAGCCGC CCAACGGAAT      60
229 CCGGTGATCC GACGTCGCAG GTTGTCGAAC CCGCCGCCGC GGAAGTATCG GTCCATGCCT     120
231 AGCCCGGCGA CGGCGAGCGC CGGAATGGCG CGAGTGAGGA GGCGGGCAAT TTGGCGGGGC     180
233 CCGGCGACGG NGAGCGCCGG AATGGCGCGA GTGAGGAGGT GGNCAGTCAT GCCCAGNGTG     240
235 ATCCAATCAA CCTGNATTCG GNCTGNGGGN CCATTTGACA ATCGAGGTAG TGAGCGCAAA     300
237 TGAATGATGG AAAACGGGNG GNGACGTCCG NTGTTCTGGT GGTGNTAGGT GNCTGNCTGG     360
239 NGTNGNGGNT ATCAGGATGT TCTTCGNCGA AANCTGATGN CGAGGAACAG GGTGTNCCCG     420
241 NNANNCCNAN GGNGTCCNAN CCCNNNNTCC TCGNCGANAT CANANAGNCG NTTGATGNGA     480
243 NAAAAGGGTG GANCAGNNNN AANTNGNGGN CCNAANAANC NNNANNGNNG NNAGNTNGNT     540
245 NNNTNTTNNC ANNNNNNNTG NNGNNGNNCN NNNCAANCNN NTNNNNGNAA NNGGNTTNTT     600
247 NAAT                                                                604
250 (2) INFORMATION FOR SEQ ID NO: 6:
252      (i) SEQUENCE CHARACTERISTICS:
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Input Set : A:\-85-6-1.app
Output Set: N:\CRF3\10242001\I724685.raw

(A) LENGTH: 633 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

TTGCANGTCG AACCACCTCA CTAAAGGGAA CAAAAGCTNG AGCTCCACCG CGGTGGCGGC 60
CGCTCTAGAA CTAGTGKATM YYYCKGGCTG CAGSAATYCG GYACGAGCAT TAGGACAGTC 120
TAACGGTCCT GTTACGGTGA TCGAATGACC GACGACATCC TGCTGATCGA CACCGACGAA 180
CGGGTGCGAA CCCTCACCCT CAACCGGCCG CAGTCCCGYA ACGCGCTCTC GGCGGCGCTA 240
CGGGATCGGT TTTTCGCGGY GTTGGYCGAC GCCGAGGYCG ACGACGACAT CGACGTCGTC 300
ATCCTCACCG GYGCCGATCC GGTGTTCTGC GCCGGACTGG ACCTCAAGGT AGCTGGCCGG 360
GCAGACCGCG CTGCCGGACA TCTCACCGCG GTGGGCGGCC ATGACCAAGC CGGTGATCGG 420
CGCGATCAAC GGCGCCGCGG TCACCGGCGG GCTCGAACTG GCGCTGTACT GCGACATCCT 480
GATCGCCTCC GAGCACGCCC GCTTCGNCGA CACCCACGCC CGGGTGGGGC TGCTGCCCAC 540
CTGGGGACTC AGTGTGTGCT TGCCGCAAAA GGTCGGCATC GGNCTGGGCC GGTGGATGAG 600
CCTGACCGGC GACTACCTGT CCGTGACCGA CGC 633

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1362 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CGACGACGAC GGCGCCGGAG AGCGGGCGCG AACGGCGATC GACGCGGCCC TGGCCAGAGT 60
CGGCACCACC CAGGAGGGAG TCGAATCATG AAATTTGTCA ACCATATTGA GCCCGTCGCG 120
CCCCGCCGAG CCGGCGGCGC GGTCGCCGAG GTCTATGCCG AGGCCCGCCG CGAGTTCGGC 180
CGGCTGCCCG AGCCGCTCGC CATGCTGTCC CCGGACGAGG GACTGCTCAC CGCCGGCTGG 240
GCGACGTTGC GCGAGACACT GCTGGTGGGC CAGGTGCCGC GTGGCCGCAA GGAAGCCGTC 300
GCCGCCGCCG TCGCGGCCAG CCTGCGCTGC CCCTGGTGCG TCGACGCACA CACCACCATG 360
CTGTACGCGG CAGGCCAAAC CGACACCGCC GCGGCGATCT TGGCCGGCAC AGCACCTGCC 420
GCCGGTGACC CGAACGCGCC GTATGTGGCG TGGGCGGCAG GAACCGGGAC ACCGGCGGGA 480
CCGCCGGCAC CGTTCGGCCC GGATGTCGCC GCCGAATACC TGGGCACCGC GGTGCAATTC 540
CACTTCATCG CACGCCTGGT CCTGGTGCTG CTGGACGAAA CCTTCCTGCC GGGGGGCCCG 600
CGCGCCCAAC AGCTCATGCG CCGCGCCGGT GGACTGGTGT TCGCCCGCAA GGTGCGCGCG 660
GAGCATCGGC CGGGCCGCTC CACCCGCCGG CTCGAGCCGC GAACGCTGCC CGACGATCTG 720
GCATGGGCAA CACCGTCCGA GCCCATAGCA ACCGCGTTCG CCGCGCTCAG CCACCACCTG 780
GACACCGCGC CGCACCTGCC GCCACCGACT CGTCAGGTGG TCAGGCGGGT CGTGGGGTCG 840
TGGCACGGCG AGCCAATGCC GATGAGCAGT CGCTGGACGA ACGAGCACAC CGCCGAGCTG 900
CCCGCCGACC TGCACGCGCC CACCCGTCTT GCCCTGCTGA CCGGCCTGGC CCCGCATCAG 960
GTGACCGACG ACGACGTCGC CGCGGCCCGA TCCCTGCTCG ACACCGATGC GGCGCTGGTT 1020
GGCGCCCTGG CCTGGGCCGC CTTCACCGCC GCGCGGCGCA TCGGCACCTG GATCGGCGCC 1080
GCCGCCGAGG GCCAGGTGTC GCGGCAAAAC CCGACTGGGT GAGTGTGCGC GCCCTGTCGG 1140
TAGGGTGTCA TCGCTGGCCC GAGGGATCTC GCGGCGGCGA ACGGAGGTGG CGACACAGGT 1200
GGAAGCTGCG CCCACTGGCT TGCGCCCCAA CGCCGTCGTG GGCGTTCGGT TGGCCGCACT 1260
GGCCGATCAG GTCGGCGCCG GCCCTTGGCC GAAGGTCCAG CTCAACGTGC CGTCACCGAA 1320
GGACCGGACG GTCACCGGGG GTCACCCTGC GCGCCCAAGG AA 1362

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1458 base pairs

RAW SEQUENCE LISTING DATE: 10/24/2001
PATENT APPLICATION: US/09/724,685 TIME: 12:35:47

Input Set : A:\-85-6-1.app
Output Set: N:\CRF3\10242001\I724685.raw

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GCGACGACCC CGATATGCCG GGCACCGTAG CGAAAGCCGT CGCCGACGCA CTCGGGCGCG 60
GTATCGCTCC CGTTGAGGAC ATTCAGGACT GCGTGGAGGC CCGGCTGGGG GAAGCCGGTC 120
TGGATGACGT GGCCCGTGTT TACATCATCT ACCGGCAGCG GCGCGCCGAG CTGCGGACGG 180
CTAAGGCCTT GCTCGGCGTG CGGGACGAGT TAAAGCTGAG CTTGGCGGCC GTGACGGTAC 240
TGCGCGAGCG CTATCTGCTG CACGACGAGC AGGGCCGGCC GGCCGAGTCG ACCGGCGAGC 300
TGATGGACCG ATCGGCGCGC TGTGTCGCGG CGGCCGAGGA CCAGTATGAG CCGGGCTCGT 360
CGAGGCGGTG GGCCGAGCGG TTCGCCACGC TATTACGCAA CCTGGAATTC CTGCCGAATT 420
CGCCCACGTT GATGAACTCT GGCACCGACC TGGGACTGCT CGCCGGCTGT TTTGTTCTGC 480
CGATTGAGGA TTCGCTGCAA TCGATCTTTG CGACGCTGGG ACAGGCCGCC GAGCTGCAGC 540
GGGCTGGAGG CGGCACCGGA TATGCGTTCA GCCACCTGCG ACCCGCCGGG GATCGGGTGG 600
CCTCCACGGG CGGCACGGCC AGCGGACCGG TGTCGTTTCT ACGGCTGTAT GACAGTGCCG 660
CGGGTGTGGT CTCCATGGGC GGTCGCCGGC GTGGCGCCTG TATGGCTGTG CTTGATGTGT 720
CGCACCCGGA TATCTGTGAT TTCGTCACCG CCAAGGCCGA ATCCCCCAGC GAGCTCCCGC 780
ATTTCAACCT ATCGGTTGGT GTGACCGACG CGTTCCTGCG GGCCGTCGAA CGCAACGGCC 840
TACACCGGCT GGTCAATCCG CGAACCGGCA AGATCGTCGC GCGGATGCCC GCCGCCGAGC 900
TGTTCGACGC CATCTGCAAA GCCGCGCACG CCGGTGGCGA TCCCGGGCTG GTGTTTCTCG 960
ACACGATCAA TAGGGCAAAC CCGGTGCCGG GGAGAGGCCG CATCGAGGCG ACCAACCCGT 1020
GCGGGGAGGT CCCACTGCTG CCTTACGAGT CATGTAATCT CGGCTCGATC AACCTCGCCC 1080
GGATGCTCGC CGACGGTCGC GTCGACTGGG ACCGGCTCGA GGAGGTCGCC GGTGTGGCGG 1140
TGCGGTTCCT TGATGACGTC ATCGATGTCA GCCGCTACCC CTTCCCCGAA CTGGGTGAGG 1200
CGGCCCGCGC CACCCGCAAG ATCGGGCTGG GAGTCATGGG TTTGGCGGAA CTGCTTGCCG 1260
CACTGGGTAT TCCGTACGAC AGTGAAGAAG CCGTGCGGTT AGCCACCCGG CTCATGCGTC 1320
GCATACAGCA GGCGGCGCAC ACGGCATCGC GGAGGCTGGC CGAAGAGCGG GGCGCATTCC 1380
CGGCGTTCAC CGATAGCCGG TTCGCGCGGT CGGGCCCGAG GCGCAACGCA CAGGTCACCT 1440
CCGTCGCTCC GACGGGCA 1458

(2) INFORMATION FOR SEQ ID NO: 9:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 862 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

ACGGTGTAAT CGTGCTGGAT CTGGAACCGC GTGGCCCGCT ACCTACCGAG ATCTACTGGC 60
GGCGCAGGGG GCTGGCCCTG GGCATCGCGG TCGTCGTAGT CGGGATCGCG GTGGCCATCG 120
TCATCGCCTT CGTCGACAGC AGCGCCGGTG CCAAACCGGT CAGCGCCGAC AAGCCGGCCT 180
CCGCCCAGAG CCATCCGGGC TCGCCGGCAC CCCAAGCACC CCAGCCGGCC GGGCAAACCG 240
AAGGTAACGC CGCCGCGGCC CCGCCGCAGG GCCAAAACCC CGAGACACCC ACGCCCACCG 300
CCGCGGTGCA GCCGCCGCCG GTGCTCAAGG AAGGGGACGA TTGCCCCGAT TCGACGCTGG 360
CCGTCAAAGG TTTGACCAAC GCGCCGCAGT ACTACGTCGG CGACCAGCCG AAGTTCACCA 420
TGGTGGTCAC CAACATCGGC CTGGTGTCCT GTAAACGCGA CGTTGGGGCC GCGGTGTTGG 480
CCGCCTACGT TTACTCGCTG GACAACAAGC GGTTGTGGTC CAACCTGGAC TGCGCGCCCT 540
CGAATGAGAC GCTGGTCAAG ACGTTTTCCC CCGGTGAGCA GGTAACGACC GCGGTGACCT 600
GGACCGGGAT GGGATCGGCG CCGCGCTGCC CATTGCCGCG GCCGGCGATC GGGCCGGGCA 660
CCTACAATCT CGTGGTACAA CTGGGCAATC TGCGCTCGCT GCCGGTTCCG TTCATCCTGA 720
ATCAGCCGCC GCCGCCGCCC GGGCCGGTAC CCGCTCCGGG TCCAGCGCAG GCGCCTCCGC 780

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

old format
O.K.

VERIFICATION SUMMARY DATE: 10/24/2001
PATENT APPLICATION: US/09/724,685 TIME: 12:35:48

Input Set : A:\-85-6-1.app
Output Set: N:\CRF3\10242001\I724685.raw

L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:1894 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54
L:1955 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58
L:1969 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:59
L:1999 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:61
L:2063 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63
L:2151 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:65
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